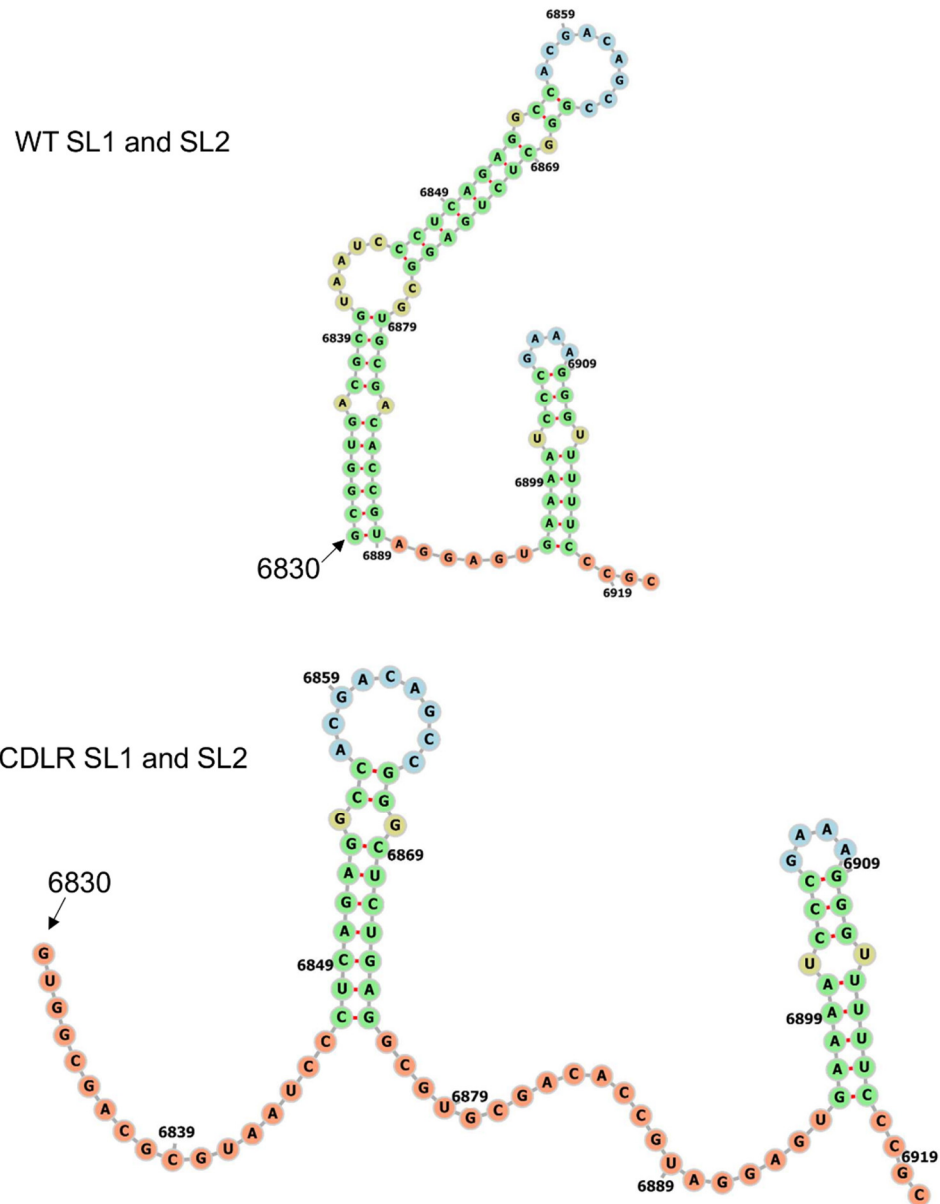


Supplementary Figure S3



RNA structure for the whole genome of the WT replicon and a replicon with the $\Delta 1D-3D_3$ encoding region permuted by the CDLR algorithm was predicted using RNAfold. The predicted structure of SL1 and SL2 stem-loops located in the 3' UTR was visualised using

Forna web service. Numbers correspond to the genomic positions of each replicon. Nucleotides forming stems are shown in green, interior loops in yellow, hairpin loops in blue and unpaired region in orange.